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## (54) METHOD FOR ANALYZING PROTEIN STRUCTURE

### (57)Abstract:

PURPOSE: To make it possible to analyze the structure of protein having the large molecular weight accurately by performing three-dimensional NMR measurement of  $^{15}\text{N}$ -1 different nuclides for specimen to be checked incorporating the protein labeled as  $^2\text{H}$  and  $^{15}\text{N}$ .

CONSTITUTION: Three-dimensional NMR of  $^{15}\text{N}$ -1 is performed for a specimen to be checked incorporating protein labeled as  $^2\text{H}$  and  $^{15}\text{N}$ . At first HMQC- COSY is performed. With respect to separated peak, amino-acid spin based identification is performed. Then, NOESY-HMQC is performed. The linking data of the neighboring amino acid are obtained based on the obtained spectrum. The linking data of the amino acid in NMR obtained in both measurements are compared with the arrangement of the amino acid of a known primary structure, and attribution is determined. In this way, the structure can be accurately analyzed even for the protein specimen having the large molecular weight.

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